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Mixtures of genotypes increase disease resistance in a coral nursery

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Marine infectious diseases are a leading cause of population declines globally due, in large part, to challenges in diagnosis and limited treatment options. Mitigating disease spread is particularly important for species targeted for conservation. In some systems, strategic arrangement of organisms in space can constrain disease outbreaks, however, this approach has not been used in marine restoration. Reef building corals have been particularly devastated by disease and continue to experience catastrophic population declines. We show that mixtures of genotypes (i.e., diversity) increased disease resistance in the critically endangered *Acropora cervicornis*, a species that is frequently targeted for restoration of degraded reefs in the broader Caribbean region. This finding suggests a more generalized relationship between diversity and disease and offers a viable strategy for mitigating the spread of infectious diseases in corals that likely applies to other foundation species targeted for restoration.

Infectious diseases in marine organisms are notoriously difficult to diagnose¹, and options for treatments in the field are limited and labor intensive^{2–5}. Thus, disease spread can quickly outpace treatment and lead to population decline or loss. There is a pressing need, therefore, to develop and implement strategies that can mitigate disease spread within affected populations. A promising approach relies on harnessing the ecological and evolutionary processes that influence disease transmission within and across populations. For example, in agricultural and small-scale experiments with *Daphnia*, intraspecific genotypic diversity can constrain disease spread when genotypes with varying resistances are grouped together^{6,7}. These findings have profound, although untested, implications for restoration of marine species that are vulnerable to diseases with few treatment options, like corals.

Coral reefs have been decimated by coral diseases^{8–10}, particularly in the Caribbean. The highly transmissible white band disease (WBD)¹¹, for example, led to the near complete collapse of dominant reef-building *Acropora cervicornis* and *Acropora palmata* coral populations^{8,12}. More recently, stony coral tissue loss disease (SCTLD) threatens the existence of numerous other reef-building corals around the Caribbean^{10,13,14}. While the etiology of SCTLD is still unknown, the application of antibiotics has been effective at a colony scale^{15–20}, but cannot keep pace with continued infections and reinfections on the reef scale. Marked coral population declines and localized extinction have led to increased global efforts to restore degraded tropical reefs that often involve coral nurseries²¹.

Coral nurseries support the asexual propagation of fast-growing species such as the Caribbean staghorn coral, *A. cervicornis*, and provide fragments to replenish coral depauperate areas^{21–23}. Multiple genotypes are reared in nurseries to support adaptation to future environmental conditions²³. However, ocean nursery-reared corals, like wild corals, are subject to disease outbreaks²⁴. Within a species, colonies vary in their innate immunity to diseases²⁵, yet the role of this variability on disease spread within and across populations is poorly understood.

To evaluate how genotypic diversity affects the spread of disease, we tracked an outbreak of white band disease in a coral nursery of the endangered coral species, *A. cervicornis*¹² over 5 months. We monitored 650 coral fragments attached to support structures (frames). Some frames harbored coral fragments originally from a single donor colony (single genotype) and other frames were comprised of fragments from multiple donor colonies representing different genotypes (mixture of genotypes)^{26,27}. We tracked the presence of disease on each fragment, across all frames, over five months and related disease prevalence on frames to diversity (mixed vs single

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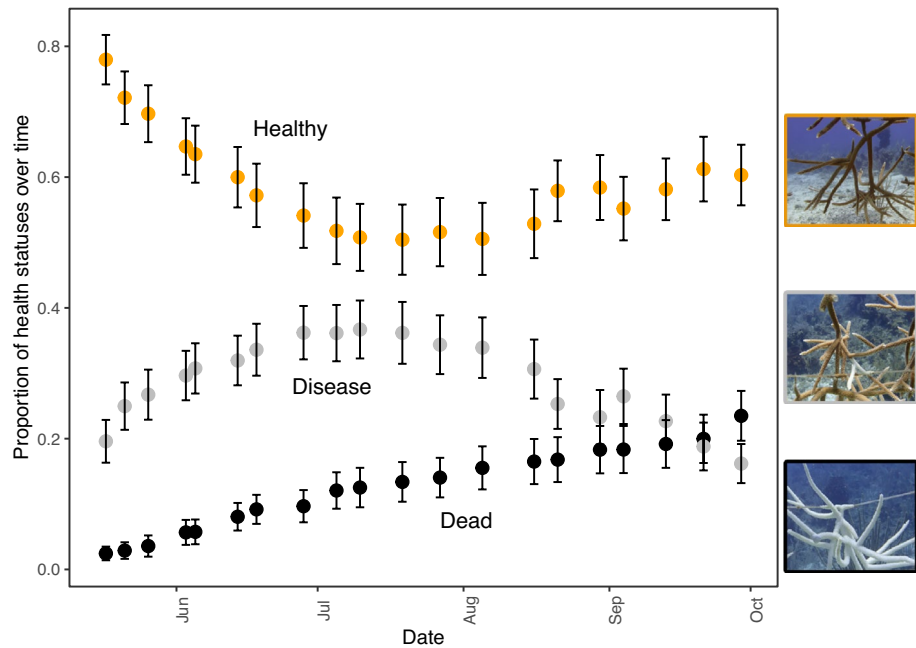


Figure 1. Mean \pm standard error (SE) of the proportions of fragments in the nursery assigned to each health category over time. Images show the appearance of corals in each category, with healthy corals showing no apparent signs of disease (outlined in orange corresponding to the orange points); diseased corals showing sloughing of tissue and a bright white skeleton left behind the lesion (outlined in gray corresponding to the gray points); and dead corals showing bright white skeletons with no tissue present and growth of algal turf (outlined in black corresponding to the black points).

genotypes on a frame). We found mixtures of genotypes on frames led to resistance of the infectious white band disease in this nursery population harboring endangered *A. cervicornis*.

Results

Disease prevalence peaked in mid-July (July 19), coincident with increasing water temperatures, and waned by the end of September 2019 (Figs. 1, S1).

Coral colonies arranged on frames with only one genotype were significantly more likely to be diseased during the peak period July (July 19) compared to frames harboring mixed genotypes (mean \pm standard error for single genotypes: $43\% \pm 0.06$ versus mixed: $26\% \pm 0.07\%$ on July 19, Fig. 2a, Model 1, $\text{Date}^2 \times \text{Diversity}$, $p < 0.001$, Table S2). Complete colony mortality was relatively low (less than 25%), although all diseased colonies showed substantial partial mortality.

Furthermore, when we compared only the genotypes found on both single and mixed frames, our results revealed intraspecific differences in disease susceptibility (Fig. 2b–f). For one genotype (G), disease prevalence was low ($< 20\%$), regardless of whether corals were on frames with mixtures of genotypes or their own genotype, indicating that this genotype was disease resistant (Fig. 2a, Model 2, $\text{Diversity} \times \text{Genotype} \times \text{Date}^2$, $p < 0.001$, Table S2). Conversely, the susceptible genotype colonies (R, Y, B) were 1.5–2 \times as likely to be diseased or die on single genotype frames than on mixed genotype frames (Figs. 2b–d, S3). One genotype appeared to be highly vulnerable no matter which frame type it was on (Fig. 2f, Genotype K), as it showed high disease prevalence on both single and mixed genotype frames.

Discussion

We documented lower disease prevalence on frames with mixed genotypes compared to frames with single genotypes. We suggest intraspecific differences in susceptibility led to these emergent population and frame-level disease progression differences on mixed and single genotype frames. Because *A. cervicornis* is known to vary in susceptibility²⁴ and resistance to WBD^{25,28,29}, it is likely that host genotypic, immunological, or microbial variation may lead to differences in disease susceptibility and contribute to the population-level disease resistance we observed. For example, the resistant genotype (G) has been previously shown to associate with a different dominant microbial variant (*Candidatus Aquarickettsia*) than the susceptible genotypes (e.g., R and Y)³⁰, which may play a role in differences in susceptibility, as suggested for other areas of the Caribbean³¹. Indeed, our results suggest that emergent population disease resistance is mediated by colony differences in disease resistance and susceptibility, which may, in turn, be mediated by key microbes.

Importantly, these results show that disease transmission is lowered on mixed frames, reducing disease spread to highly vulnerable individuals. Thus, some of the corals that are vulnerable to disease can be “rescued” by resistant genotypes (i.e., Fig. 2c–e), likely because resistant genotypes prevent the transmission of the disease between

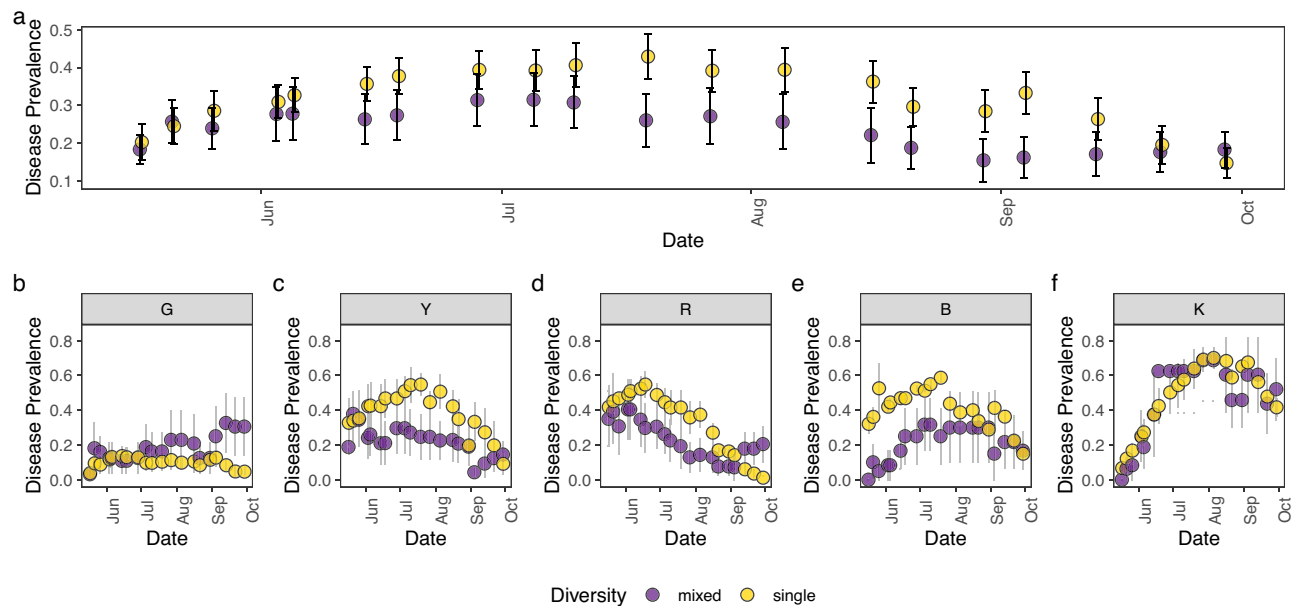


Figure 2. Prevalence of disease Mean \pm standard error (SE) of disease prevalence across (a) all frames, and by genotype (b) “G” (c) “Y”, (d) “R”, (e) “B”, (f) “K”. Point colors represent mixed (purple) and single (yellow) genotype treatments. Genotype G (plot b) and Genotypes Y, R, and B (plots c–e) are the resistant and vulnerable genotypes, respectively. Genotype K (plot f) is highly vulnerable.

fragments. In fact, when the resistant genotype (G) was present on a frame, disease prevalence (both within a genotype and a frame as whole) tended to be lower than on other mixed genotype frames when the resistant genotype was absent (Figs. 2 and S2). Frames that lacked the known resistant genotype (4 mixed genotype frames) or contained the highly susceptible genotype (K) tended to have higher disease prevalence, indicating (a) disease resistance is rare, (b) there may be a threshold in which the presence of a disease resistant genotype no longer resists disease, and/or (c) there are some highly susceptible genotypes that amplify disease. These hypotheses require further testing. In general, on mixed frames, corals from resistant genotypes rescue disease-vulnerable genotypes. The maintenance of the susceptible genotypes in the population allows for a broader suite of genotypes to remain in the genetic pool, which increases adaptive resilience to changing environmental conditions beyond disease²³. Our results also highlight that because disease resistance is a cryptic and rare trait³², increasing genotypic diversity in nurseries increases the likelihood of diluting the disease³³.

This finding has important implications for wild coral populations, particularly those that already exhibit low numbers of colonies and reduced genetic variability³⁴. Specifically, our results suggest that the prevalence of disease will increase across the Caribbean as genotypic diversity is lost and the likelihood of the diluting effects of resistant genotypes are diminished. Residual populations although comprised of disease resistant genotypes may lack the full complement of genetic traits necessary to support selective processes that give rise to adaptation and evolution²³.

Our work adds to the literature suggesting that diversity can reduce the spread of infectious diseases by distributing pathogens across non-viable hosts, i.e. a dilution effect³⁵. Low genetic diversity has been correlated with increased disease prevalence^{35–38} for mammals^{39,40}, frogs⁴¹, invertebrates^{7,42}, and plants^{6,43,44}. We suggest the linkage between diversity and disease is even more general than we have previously realized. Here, we highlight this relationship in a marine system: between an infectious disease and mixtures of genotypes in endangered corals. The ecological and evolutionary phenomena that underpin our findings for *A. cervicornis* have broader conservation consequences, and we suggest incorporating aggregations of diverse genotypes when restoring corals, and other marine species, particularly those vulnerable to infectious diseases.

Methods

Nursery design. We monitored 650 individual corals in an ocean-based nursery offshore of the Central Caribbean Marine Institute (CCMI) on Little Cayman Island, Cayman Islands. The nursery was at a depth of 18 m. This nursery supplies coral colonies for re-populating nearby reefs, similar to many other coral nurseries around the Caribbean and the world^{21–23,45}. In general, nurseries rely on repeated fragmenting of corals to create numerous clones from a single donor colony. The resulting coral fragments are then suspended in the water column on structures within the nursery and allowed to grow before being placed on reefs, a process referred to as outplanting²¹. Corals in the CCMI nursery were attached to PVC frames using monofilament line that was secured with crimps. Frames were 3-m wide and 1.5-m high. The structures were anchored using ropes tied to cinderblocks and held upright by empty plastic jugs partially filled with compressed air. Frames were ~1–3 m away from any other frame (see Fig. S2).

Because genotypic diversity is critical for populations to adapt to changing conditions, multiple genotypes (i.e., fragments from multiple donor colonies) are grown in nurseries to enhance genetic diversity of outplanted colonies and improve resilience of local populations. The CCMI nursery was established in 2012, and it started with five fragments collected from five colonies at three locations around Little Cayman Island. After collection, the donor colonies were determined to be genetically distinct via Genotyping by Sequencing (GBS) to produce single nucleotide polymorphisms (SNPs)²⁶. These colonies were color coded and denoted by abbreviations: Blue (B), Green (G), Red (R), Yellow (Y), Black (K). These colonies also show genotypic variation in growth²⁷ and microbial communities (from colonies in the G, Y and R genotypes)³⁰. We collected nine additional fragments from isolated colonies in nine locations in 2016. We consider these fragments different genotypes based on colony isolation and the high degree of small-scale genetic diversity reported for *A. cervicornis*^{23,26,46}. Thus, the nursery was considered to contain 14 genotypes at the onset of the disease (see Table S1 for names and which frames genotypes were on).

We arranged fragments on either mixed ($n = 13$) or single genotype frames ($n = 17$), with ~ 30 cm between each fragment. Each frame contained 5–50 corals (Fig. S2, Table S1). Each of the single genotype frames was populated by one of the original 5 genotypes. Mixed frames contained 3–8 genotypes per frame. The genotypic identity of individual colonies suspended on the frames was tracked with colored beads threaded on the monofilament above the crimp used to secure the fragment on the frame (Fig. S2, Table S1). Here, we used the abbreviations of the colors for simplicity.

Disease monitoring. Starting in spring (May) 2019, while on a routine cleaning of the nursery, divers noticed sloughing of tissue along disease fronts that progressed toward the tips of the fragments. The symptoms of the disease characterized it as an acute tissue loss syndrome that matched the descriptions of White Band Disease Type I and rapid tissue loss disease⁴, which visually are both identified as White Band Disease⁴⁷ or WBD. We also recovered putative WBD pathogen *Vibrio harveyi* in diseased tissues⁴⁸ (Schul et al. in review). Previously, this disease was implicated in decimating populations of the critically endangered coral, *A. cervicornis*. WBD is highly infectious, and can spread through coral-coral contact as well as through waterborne transmission¹¹.

We began monitoring the disease on 17 May 2019 and ceased on 29 September 2019. Weekly, divers monitored each of the fragments in the nursery, visually assessing their health status. The health of the different fragments was recorded as: Healthy (no disease apparent), Diseased (presence of disease identified by sloughing tissue), or Dead (bright white skeleton with no tissue and presence of small filamentous turf algae, Fig. 1). When we observed recovery of diseased fragments, characterized by tissue growing onto a dead skeleton, the status of the colony was revised to “Healthy.” Across the whole monitoring period, 70% of colonies (453) in the nursery showed signs of disease during two or more sampling events. Complete coral mortality was relatively low (less than 25%), although all diseased corals showed substantial partial mortality. Nearly 500 colonies (more than 75% of the nursery) recovered or were unaffected by the disease.

Analysis

To model the prevalence of disease on frames containing mixed vs single genotypes across all of the fragments in the nursery, we applied a mixed effects binomial model calculated in R (v 4.0.0) using glmTMBB⁴⁹, and car packages⁵⁰ on the counts of disease versus the counts of not diseased (healthy and dead) corals. The model treated Diversity as a fixed effect (colonies on a single or mixed genotype frame), Date (date of sampling) as a quadratic fixed effect to capture the dynamics of the disease, and a random intercept for the frame sampled (Model 1: $\text{Date}^2 \times \text{Diversity} + \text{Density} + (1|\text{Frame})$) to account for the repeated sampling of fragments on frames, and effects associated with the frame. We also included an interaction term, expecting the number of diseased corals to change over time, and that this would depend on whether corals were on single versus mixed frames. We included density of corals on the frame as a fixed effect. Assumptions were tested by simulating and testing the outliers of the residuals of the binomial model (DHARMA package).

To understand the interactive effects of genotype and diversity, we also applied a model to the data for the five genotypes that were present on both single and mixed frames. This model included Diversity as a fixed effect (single vs mixed); Genotype as a fixed effect (B, R, K, Y, and G), a quadratic fixed effect for Date (Model 2: $\text{Date}^2 \times \text{Genotype} \times \text{Diversity} + \text{Density} + (1|\text{Frame})$), and a random intercept for the frame sampled, again accounting for the repeated sampling of the frames. We also included density as a fixed effect.

Data availability

The datasets generated during the current study are available in the Dryad repository: Brown, Anya et al. (2022), CCMI nursery coral disease 2019, Dryad, Dataset, <https://doi.org/10.25338/B8F643>. The code is available at: https://github.com/anyabrown/coral_nursery_disease_frames

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References

- Vega Thurber, R. et al. Deciphering coral disease dynamics: Integrating host, microbiome, and the changing environment. *Front. Ecol. Evol.* **2020**, 8 (2020).
- Groner, M. L. et al. Managing marine disease emergencies in an era of rapid change. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* **371**, 1689 (2016).
- Richardson, L. L. Coral diseases: What is really known?. *Trends Ecol. Evol.* **13**, 438–443 (1998).
- Miller, M. W., Lohr, K. E., Cameron, C. M., Williams, D. E. & Peters, E. C. Disease dynamics and potential mitigation among restored and wild staghorn coral, *Acropora cervicornis*. *PeerJ* <https://doi.org/10.7287/peerj.preprints.328> (2014).

5. Teplitski, M. & Ritchie, K. How feasible is the biological control of coral diseases?. *Trends Ecol. Evol.* **24**, 378–385 (2009).
6. Zhu, Y. *et al.* Genetic diversity and disease control in rice. *Nature* **406**, 718–722 (2000).
7. Altermatt, F. & Ebert, D. Genetic diversity of *Daphnia magna* populations enhances resistance to parasites. *Ecol. Lett.* **11**, 918–928 (2008).
8. Aronson, R. B. & Precht, W. F. White-band disease and the changing face of Caribbean coral reefs. In (ed Porter, J. W.) *The Ecology and Etiology of Newly Emerging Marine Diseases* 25–38 (Springer Netherlands, 2001).
9. Ruiz-Moreno, D. *et al.* Global coral disease prevalence associated with sea temperature anomalies and local factors. *Dis. Aquat. Organ.* **100**, 249–261 (2012).
10. Precht, W. F., Gintert, B. E., Robbart, M. L., Fura, R. & van Woesik, R. Unprecedented disease-related coral mortality in Southeastern Florida. *Sci. Rep.* **6**, 31374 (2016).
11. Gignoux-Wolfsohn, S. A., Marks, C. J. & Vollmer, S. V. White Band Disease transmission in the threatened coral, *Acropora cervicornis*. *Sci. Rep.* **2**, 804 (2012).
12. Aronson, R., Bruckner, A., Moore, J., Precht, B. & Weil, E. *Acropora cervicornis*. IUCN Red List of Threatened Species <https://doi.org/10.2305/iucn.uk.2008.rlts.t133381a3716457.en> (2008).
13. Alvarez-Filip, L., González-Barríos, F. J., Pérez-Cervantes, E., Molina-Hernández, A. & Estrada-Saldívar, N. Stony coral tissue loss disease decimated Caribbean coral populations and reshaped reef functionality. *Commun. Biol.* **5**, 440 (2022).
14. Heres, M. M., Farmer, B. H., Elmer, F. & Hertler, H. Ecological consequences of Stony Coral Tissue Loss Disease in the Turks and Caicos Islands. *Coral Reefs* **40**, 609–624 (2021).
15. Neely, K. L., Shea, C. P., Macaulay, K. A., Hower, E. K. & Dobler, M. A. Short- and long-term effectiveness of coral disease treatments. *Front. Mar. Sci.* **2021**, 8 (2021).
16. Neely, K. L., Macaulay, K. A., Hower, E. K. & Dobler, M. A. Effectiveness of topical antibiotics in treating corals affected by stony coral tissue loss disease. *PeerJ* **8**, e9289 (2020).
17. Shilling, E. N., Combs, I. R. & Voss, J. D. Assessing the effectiveness of two intervention methods for stony coral tissue loss disease on *Montastraea cavernosa*. *Sci. Rep.* **11**, 8566 (2021).
18. Walker, B. K., Turner, N. R., Noren, H. K. G., Buckley, S. F. & Pitts, K. A. Optimizing stony coral tissue loss disease (SCTLD) intervention treatments on *Montastraea cavernosa* in an Endemic Zone. *Front. Mar. Sci.* **8**, 666224 (2021).
19. Forrester, G. E., Arton, L., Horton, A., Nickles, K. & Forrester, L. M. Antibiotic treatment ameliorates the impact of stony coral tissue loss disease (SCTLD) on coral communities. *Front. Mar. Sci.* **2022**, 9 (2022).
20. Lee-Hing, C. *et al.* Management responses in Belize and Honduras, as stony coral tissue loss disease expands its prevalence in the Mesoamerican reef. *Front. Mar. Sci.* **9**, 1 (2022).
21. Young, C. N., Schopmeyer, S. A. & Lirman, D. A review of reef restoration and coral propagation using the threatened genus *Acropora* in the Caribbean and Western Atlantic. *Bull. Mar. Sci.* **88**, 1075–1098 (2012).
22. Lirman, D. & Schopmeyer, S. Ecological solutions to reef degradation: Optimizing coral reef restoration in the Caribbean and Western Atlantic. *PeerJ* **4**, e2597 (2016).
23. Baums, I. B. *et al.* Considerations for maximizing the adaptive potential of restored coral populations in the western Atlantic. *Ecol. Appl.* **29**, e01978 (2019).
24. Rosales, S. M. *et al.* Microbiome differences in disease-resistant vs susceptible *Acropora* corals subjected to disease challenge assays. *Sci. Rep.* **9**, 18279 (2019).
25. Pinzón, C. J. H., Beach-Letendre, J., Weil, E. & Mydlarz, L. D. Relationship between phylogeny and immunity suggests older Caribbean coral lineages are more resistant to disease. *PLoS ONE* **9**, e104787. <https://doi.org/10.1371/journal.pone.0104787> (2014).
26. Drury, C. *et al.* Genomic patterns in *Acropora cervicornis* show extensive population structure and variable genetic diversity. *Ecol. Evol.* **7**, 6188–6200 (2017).
27. Maneval, P., Jacoby, C. A., Harris, H. E. & Frazer, T. K. Genotype, nursery design, and depth influence the growth of *Acropora cervicornis* fragments. *Front. Mar. Sci.* **8**, 1 (2021).
28. Wright, R. M. *et al.* Intraspecific differences in molecular stress responses and coral pathobiome contribute to mortality under bacterial challenge in *Acropora millepora*. *Sci. Rep.* **7**, 2609 (2017).
29. Vollmer, S. V. & Kline, D. I. Natural disease resistance in threatened staghorn corals. *PLoS ONE* **3**, e3718 (2008).
30. Miller, N., Maneval, P., Manfrino, C., Frazer, T. K. & Meyer, J. L. Spatial distribution of microbial communities among colonies and genotypes in nursery-reared *Acropora cervicornis*. *PeerJ* **8**, e9635 (2020).
31. Klings, G., Maher, R. L., Vega-Thurber, R. L. & Muller, E. M. Parasitic, “*Candidatus* Aquarickettsia rohweri” is a marker of disease susceptibility in *Acropora cervicornis* but is lost during thermal stress. *Environ. Microbiol.* **22**, 5341–5355 (2020).
32. Miller, M. W. *et al.* Genotypic variation in disease susceptibility among cultured stocks of elkhorn and staghorn corals. *PeerJ* **7**, e6751 (2019).
33. Rohr, J. R. *et al.* Towards common ground in the biodiversity-disease debate. *Nat. Ecol. Evol.* **4**, 24–33 (2020).
34. Shearer, T. L., Porto, I. & Zubillaga, A. L. Restoration of coral populations in light of genetic diversity estimates. *Coral Reefs* **28**, 727–733 (2009).
35. Ostfeld, R. S. & Keesing, F. Biodiversity and disease risk: The case of Lyme disease. *Conserv. Biol.* **14**, 722–728 (2000).
36. Lively, C. M. The effect of host genetic diversity on disease spread. *Am. Nat.* **175**, E149–E152 (2010).
37. Ostfeld, R. S. & Keesing, F. Effects of host diversity on infectious disease. *Annu. Rev. Ecol. Syst.* **43**, 157–182 (2012).
38. King, K. C. & Lively, C. M. Does genetic diversity limit disease spread in natural host populations?. *Heredity* **109**, 199–203 (2012).
39. Acevedo-Whitehouse, K., Gulland, F., Greig, D. & Amos, W. Inbreeding: Disease susceptibility in California sea lions. *Nature* **422**, 35 (2003).
40. O’Brien, S. J. *et al.* Genetic basis for species vulnerability in the cheetah. *Science* **227**, 1428–1434 (1985).
41. Pearman, P. B. & Garner, T. W. J. Susceptibility of Italian agile frog populations to an emerging strain of Ranavirus parallels population genetic diversity. *Ecol. Lett.* **8**, 401–408 (2005).
42. Reber, A., Castella, G., Christe, P. & Chapuisat, M. Experimentally increased group diversity improves disease resistance in an ant species. *Ecol. Lett.* **11**, 682–689 (2008).
43. Mundt, C. C. Use of multiline cultivars and cultivar mixtures for disease management. *Annu. Rev. Phytopathol.* **40**, 381–410 (2002).
44. Elton, C. S. *The Ecology of Invasions by Animals and Plants* (University of Chicago Press, 2000).
45. Schopmeyer, S. A. *et al.* Regional restoration benchmarks for *Acropora cervicornis*. *Coral Reefs* **36**, 1047–1057 (2017).
46. Baums, I. B., Miller, M. W. & Hellberg, M. E. Geographic variation in clonal structure in a reef-building Caribbean coral, *Acropora palmata*. *Ecol. Monogr.* **76**, 503–519 (2006).
47. Gignoux-Wolfsohn, S. A., Precht, W. F., Peters, E. C., Gintert, B. E. & Kaufman, L. S. Ecology, histopathology, and microbial ecology of a white-band disease outbreak in the threatened staghorn coral *Acropora cervicornis*. *Dis. Aquat. Organ.* **137**, 217–237 (2020).
48. Gignoux-Wolfsohn, S. A. & Vollmer, S. V. Identification of candidate coral pathogens on white band disease-infected staghorn coral. *PLoS ONE* **10**, e0134416 (2015).
49. Brooks, M. *et al.* GlmmTMB balances speed and flexibility among packages for zero-inflated generalized linear mixed modeling. *R J.* **9**, 378–400 (2017).
50. Fox, J. & Weisburg, S. *An R Companion to Applied Regression* 3rd edn. (Sage, 2019).

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Author contributions

A.L.B.: conceived of project, wrote the paper, analyzed the results. D.E.A.: collected the data, set up nursery. L.S.: collected the data, set up nursery. S.M.: collected the data. M.S.: collected the data. J.M.: feedback on paper. C.M.: funding, initial set up of the nursery. T.K.F.: funding, conceived of project, feedback on paper.

Competing interests

The authors declare no competing interests.

Additional information

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